SEQUENCE LISTING

<110> TOJI, SHINGO
        YANO, MINORU
        TAMAI, KATSUYUKI

<120> THIOREDOXIN REDUCTASE II

<130> 55865-71965

<140> 09/830,706
<141> 2001-04-27

<150> PCT/JP99/05983
<151> 1999-10-28

<150> JP 1998-310422
<151> 1998-10-30

<160> 38

<170> PatentIn Ver. 2.1

<210> 1
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cgg acg cag gcc gtg gcg ggc ggg gtg cgg ggc gcg gcg cgg ggc gca   99
Arg Thr Gln Ala Val Ala Gly Gly Val Arg Gly Ala Ala Arg Gly Ala
 15   20   25   30

gca gca ggt cag cgg gac tat gat ctc ctg gtg gtc ggc ggg gga tct   147
Ala Ala Gly Gln Arg Asp Tyr Asp Leu Leu Val Val Gly Gly Gly Ser
                 35   40   45

ggt ggc ctg gct tgt gcc aag gag gcc gcc cag ctg gga agg aag gtg   195
Gly Gly Leu Ala Cys Ala Lys Glu Ala Ala Gln Leu Gly Arg Lys Val
             50   55   60

gcc gtg gtg gac tac gtg gaa cct tct ccc caa ggc acc cgg tgg ggc   243
Ala Val Val Asp Tyr Val Glu Pro Ser Pro Gln Gly Thr Arg Trp Gly
             65   70   75

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ctc ggc ggc acc tgc gtc aac gtg ggc tgc atc ccc aag aag ctg atg    291
Leu Gly Gly Thr Cys Val Asn Val Gly Cys Ile Pro Lys Lys Leu Met
     80                  85              90

cac cag gcg gca ctg ctg gga ggc ctg atc caa gat gcc ccc aac tat    339
His Gln Ala Ala Leu Leu Gly Gly Leu Ile Gln Asp Ala Pro Asn Tyr
 95              100             105                 110

ggc tgg gag gtg gcc cag ccc gtg ccg cat gac tgg agg aag atg gca    387
Gly Trp Glu Val Ala Gln Pro Val Pro His Asp Trp Arg Lys Met Ala
                115             120                 125

gaa gct gtt caa aat cac gtg aaa tcc ttg aac tgg ggc cac cgt gtc    435
Glu Ala Val Gln Asn His Val Lys Ser Leu Asn Trp Gly His Arg Val
            130             135                 140

cag ctt cag gac aga aaa gtc aag tac ttt aac atc aaa gcc agc ttt    483
Gln Leu Gln Asp Arg Lys Val Lys Tyr Phe Asn Ile Lys Ala Ser Phe
        145                 150             155

gtt gac gag cac acg gtt tgc ggc gtt gcc aaa ggt ggg aaa gag att    531
Val Asp Glu His Thr Val Cys Gly Val Ala Lys Gly Gly Lys Glu Ile
        160             165                 170

ctg ctg tca gcc gat cac atc atc att gct act gga ggg cgg ccg aga    579
Leu Leu Ser Ala Asp His Ile Ile Ile Ala Thr Gly Gly Arg Pro Arg
175             180                 185                 190

tac ccc acg cac atc gaa ggt gcc ttg gaa tat gga atc aca agt gat    627
Tyr Pro Thr His Ile Glu Gly Ala Leu Glu Tyr Gly Ile Thr Ser Asp
                195                 200             205

gac atc ttc tgg ctg aag gaa tcc cct gga aaa acg ttg gtg gtc ggg    675
Asp Ile Phe Trp Leu Lys Glu Ser Pro Gly Lys Thr Leu Val Val Gly
            210                 215             220

gcc agc tat gtg gcc ctg gag tgt gct ggc ttc ctc acc ggg att ggg    723
Ala Ser Tyr Val Ala Leu Glu Cys Ala Gly Phe Leu Thr Gly Ile Gly
        225                 230             235

ctg gac acc acc atc atg atg cgc agc atc ccc ctc cgc ggc ttc gac    771
Leu Asp Thr Thr Ile Met Met Arg Ser Ile Pro Leu Arg Gly Phe Asp
        240                 245             250

cag caa atg tcc tcc atg gtc ata gag cac atg gca tct cat ggc acc    819
Gln Gln Met Ser Ser Met Val Ile Glu His Met Ala Ser His Gly Thr
255                 260                 265                 270

cgg ttc ctg agg ggc tgt gcc ccc tcg cgg gtc agg agg ctc cct gat    867
Arg Phe Leu Arg Gly Cys Ala Pro Ser Arg Val Arg Arg Leu Pro Asp
                275                 280                 285

ggc cag ctg cag gtc acc tgg gag gac agc acc acc ggc aag gag gac    915
Gly Gln Leu Gln Val Thr Trp Glu Asp Ser Thr Thr Gly Lys Glu Asp
            290                 295                 300
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acg ggc acc ttt gac acc gtc ctg tgg gcc ata ggt cga gtc cca gac   963
Thr Gly Thr Phe Asp Thr Val Leu Trp Ala Ile Gly Arg Val Pro Asp
        305                 310             315

acc aga agt ctg aat ttg gag aag gct ggg gta gat act agc ccc gac  1011
Thr Arg Ser Leu Asn Leu Glu Lys Ala Gly Val Asp Thr Ser Pro Asp
        320                 325             330

act cag aag atc ctg gtg gac tcc cgg gaa gcc acc tct gtg ccc cac  1059
Thr Gln Lys Ile Leu Val Asp Ser Arg Glu Ala Thr Ser Val Pro His
335                 340             345                 350

atc tac gcc att ggt gac gtg gtg gag ggg cgg cct gag ctg aca ccc  1107
Ile Tyr Ala Ile Gly Asp Val Val Glu Gly Arg Pro Glu Leu Thr Pro
                355             360             365

aca gcg atc atg gcc ggg agg ctc ctg gtg cag cgg ctc ttc ggc ggg  1155
Thr Ala Ile Met Ala Gly Arg Leu Leu Val Gln Arg Leu Phe Gly Gly
            370             375             380

tcc tca gat ctg atg gac tac gac aat gtt ccc acg acc gtc ttc acc  1203
Ser Ser Asp Leu Met Asp Tyr Asp Asn Val Pro Thr Thr Val Phe Thr
        385             390             395

cca ctg gag tat ggc tgt gtg ggg ctg tcc gag gag gag gca gtg gct  1251
Pro Leu Glu Tyr Gly Cys Val Gly Leu Ser Glu Glu Glu Ala Val Ala
    400             405             410

cgc cac ggg cag gag cat gtt gag gtc tat cac gcc cat tat aaa cca  1299
Arg His Gly Gln Glu His Val Glu Val Tyr His Ala His Tyr Lys Pro
415             420             425             430

ctg gag ttc acg gtg gct gga cga gat gca tcc cag tgt tat gta aag  1347
Leu Glu Phe Thr Val Ala Gly Arg Asp Ala Ser Gln Cys Tyr Val Lys
            435             440             445

atg gtg tgc ctg agg gag ccc cca cag ctg gtg ctg ggc ctg cat ttc  1395
Met Val Cys Leu Arg Glu Pro Pro Gln Leu Val Leu Gly Leu His Phe
            450             455             460

ctt ggc ccc aac gca ggc gaa gtt act caa gga ttt gct ctg ggg atc  1443
Leu Gly Pro Asn Ala Gly Glu Val Thr Gln Gly Phe Ala Leu Gly Ile
        465             470             475

aag tgt ggg gct tcc tat gcg cag gtg atg cgg acc gtg ggt atc cat  1491
Lys Cys Gly Ala Ser Tyr Ala Gln Val Met Arg Thr Val Gly Ile His
        480             485             490

ccc aca tgc tct gag gag gta gtc aag ctg cgc atc tcc aag cgc tca  1539
Pro Thr Cys Ser Glu Glu Val Val Lys Leu Arg Ile Ser Lys Arg Ser
495                 500             505                 510

ggc ctg gac ccc acg gtg aca ggc tgc tga ggg taagcgccat ccctgcaggc 1592
Gly Leu Asp Pro Thr Val Thr Gly Cys Xaa Gly
            515             520

cagggcacac ggtgcgcccg ccgccagctc ctcggaggcc agacccagga tggctgcagg 1652
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ccaggtttgg ggggcctcaa ccctctcctg gagcgcctgt gagatggtca gcgtggagcg 1712

caagtgctgg acgggtggcc cgtgtgcccc acagggatgg ctcaggggac tgtccacctc 1772

acccctgcac ctttcagcct ttgccgccgg gcaccccccc caggctcctg gtgccggatg 1832

atgacgacct gggtggaaac ctaccctgtg ggcacccatg tccgagcccc ctggcatttc 1892

tgcaatgcaa ataaagaggg tacttttct gaagtgtgta aaaaaaaaa aaaaaaaaa 1952

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<400> 2

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            20                  25                  30

Gly Gln Arg Asp Tyr Asp Leu Leu Val Val Gly Gly Gly Ser Gly Gly
         35                  40                  45

Leu Ala Cys Ala Lys Glu Ala Ala Gln Leu Gly Arg Lys Val Ala Val
     50                  55                  60

Val Asp Tyr Val Glu Pro Ser Pro Gln Gly Thr Arg Trp Gly Leu Gly
 65                  70                  75                  80

Gly Thr Cys Val Asn Val Gly Cys Ile Pro Lys Lys Leu Met His Gln
                 85                  90                  95

Ala Ala Leu Leu Gly Gly Leu Ile Gln Asp Ala Pro Asn Tyr Gly Trp
             100                 105                 110

Glu Val Ala Gln Pro Val Pro His Asp Trp Arg Lys Met Ala Glu Ala
            115                 120                 125

Val Gln Asn His Val Lys Ser Leu Asn Trp Gly His Arg Val Gln Leu
        130                 135                 140

Gln Asp Arg Lys Val Lys Tyr Phe Asn Ile Lys Ala Ser Phe Val Asp
145                 150                 155                 160

Glu His Thr Val Cys Gly Val Ala Lys Gly Gly Lys Glu Ile Leu Leu
                165                 170                 175
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Ser Ala Asp His Ile Ile Ile Ala Thr Gly Gly Arg Pro Arg Tyr Pro
        180   185   190

Thr His Ile Glu Gly Ala Leu Glu Tyr Gly Ile Thr Ser Asp Asp Ile
        195   200   205

Phe Trp Leu Lys Glu Ser Pro Gly Lys Thr Leu Val Val Gly Ala Ser
    210   215   220

Tyr Val Ala Leu Glu Cys Ala Gly Phe Leu Thr Gly Ile Gly Leu Asp
225   230   235   240

Thr Thr Ile Met Met Arg Ser Ile Pro Leu Arg Gly Phe Asp Gln Gln
            245   250   255

Met Ser Ser Met Val Ile Glu His Met Ala Ser His Gly Thr Arg Phe
            260   265   270

Leu Arg Gly Cys Ala Pro Ser Arg Val Arg Arg Leu Pro Asp Gly Gln
        275   280   285

Leu Gln Val Thr Trp Glu Asp Ser Thr Thr Gly Lys Glu Asp Thr Gly
    290   295   300

Thr Phe Asp Thr Val Leu Trp Ala Ile Gly Arg Val Pro Asp Thr Arg
305   310   315   320

Ser Leu Asn Leu Glu Lys Ala Gly Val Asp Thr Ser Pro Asp Thr Gln
            325   330   335

Lys Ile Leu Val Asp Ser Arg Glu Ala Thr Ser Val Pro His Ile Tyr
            340   345   350

Ala Ile Gly Asp Val Val Glu Gly Arg Pro Glu Leu Thr Pro Thr Ala
        355   360   365

Ile Met Ala Gly Arg Leu Leu Val Gln Arg Leu Phe Gly Gly Ser Ser
    370   375   380

Asp Leu Met Asp Tyr Asp Asn Val Pro Thr Thr Val Phe Thr Pro Leu
385   390   395   400

Glu Tyr Gly Cys Val Gly Leu Ser Glu Glu Glu Ala Val Ala Arg His
            405   410   415

Gly Gln Glu His Val Glu Val Tyr His Ala His Tyr Lys Pro Leu Glu
        420   425   430

Phe Thr Val Ala Gly Arg Asp Ala Ser Gln Cys Tyr Val Lys Met Val
    435   440   445

Cys Leu Arg Glu Pro Pro Gln Leu Val Leu Gly Leu His Phe Leu Gly
    450   455   460

Pro Asn Ala Gly Glu Val Thr Gln Gly Phe Ala Leu Gly Ile Lys Cys
465   470   475   480

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Gly Ala Ser Tyr Ala Gln Val Met Arg Thr Val Gly Ile His Pro Thr
            485                 490                 495

Cys Ser Glu Glu Val Val Lys Leu Arg Ile Ser Lys Arg Ser Gly Leu
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Asp Pro Thr Val Thr Gly Cys Xaa Gly
        515                 520


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<213> Homo sapiens

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ttctccatcc ctcctttttt tggctgcccc ttgcctgcct tcctcgccag tagcttgcag  120

agtagacacg atgacacctt ttgcaggcta aaaaggctga gagtggcact atgtgcagtg  180

agccacc atg gag gac caa gca ggt cag cgg gac tat gat ctc ctg gtg     229
        Met Glu Asp Gln Ala Gly Gln Arg Asp Tyr Asp Leu Leu Val
          1           5                   10

gtc ggc ggg gga tct ggt ggc ctg gct tgt gcc aag gag gcc gcc cag     277
Val Gly Gly Gly Ser Gly Gly Leu Ala Cys Ala Lys Glu Ala Ala Gln
 15                  20                  25                  30

ctg gga agg aag gtg gcc gtg gtg gac tac gtg gaa cct tct ccc caa     325
Leu Gly Arg Lys Val Ala Val Val Asp Tyr Val Glu Pro Ser Pro Gln
                 35                  40                  45

ggc acc cgg tgg ggc ctc ggc ggc acc tgc gtc aac gtg ggc tgc atc     373
Gly Thr Arg Trp Gly Leu Gly Gly Thr Cys Val Asn Val Gly Cys Ile
             50                  55                  60

ccc aag aag ctg atg cac cag gcg gca ctg ctg gga ggc ctg atc caa     421
Pro Lys Lys Leu Met His Gln Ala Ala Leu Leu Gly Gly Leu Ile Gln
         65                  70                  75

gat gcc ccc aac tat ggc tgg gag gtg gcc cag ccc gtg ccg cat gac     469
Asp Ala Pro Asn Tyr Gly Trp Glu Val Ala Gln Pro Val Pro His Asp
     80                  85                  90

tgg agg aag atg gca gaa gct gtt caa aat cac gtg aaa tcc ttg aac     517
Trp Arg Lys Met Ala Glu Ala Val Gln Asn His Val Lys Ser Leu Asn
 95                 100                 105                 110
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tgg ggc cac cgt gtc cag ctt cag gac aga aaa gtc aag tac ttt aac   565
Trp Gly His Arg Val Gln Leu Gln Asp Arg Lys Val Lys Tyr Phe Asn
                115                 120                 125

atc aaa gcc agc ttt gtt gac gag cac acg gtt tgc ggc gtt gcc aaa   613
Ile Lys Ala Ser Phe Val Asp Glu His Thr Val Cys Gly Val Ala Lys
                130                 135                 140

ggt ggg aaa gag att ctg ctg tca gcc gat cac atc atc att gct act   661
Gly Gly Lys Glu Ile Leu Leu Ser Ala Asp His Ile Ile Ile Ala Thr
                145                 150                 155

gga ggg cgg ccg aga tac ccc acg cac atc gaa ggt gcc ttg gaa tat   709
Gly Gly Arg Pro Arg Tyr Pro Thr His Ile Glu Gly Ala Leu Glu Tyr
    160                 165                 170

gga atc aca agt gat gac atc ttc tgg ctg aag gaa tcc cct gga aaa   757
Gly Ile Thr Ser Asp Asp Ile Phe Trp Leu Lys Glu Ser Pro Gly Lys
175                 180                 185                 190

acg ttg gtg gtc ggg gcc agc tat gtg gcc ctg gag tgt gct ggc ttc   805
Thr Leu Val Val Gly Ala Ser Tyr Val Ala Leu Glu Cys Ala Gly Phe
                195                 200                 205

ctc acc ggg att ggg ctg gac acc acc atc atg atg cgc agc atc ccc   853
Leu Thr Gly Ile Gly Leu Asp Thr Thr Ile Met Met Arg Ser Ile Pro
                210                 215                 220

ctc cgc ggc ttc gac cag caa atg tcc tcc atg gtc ata gag cac atg   901
Leu Arg Gly Phe Asp Gln Gln Met Ser Ser Met Val Ile Glu His Met
                225                 230                 235

gca tct cat ggc acc cgg ttc ctg agg ggc tgt gcc ccc tcg cgg gtc   949
Ala Ser His Gly Thr Arg Phe Leu Arg Gly Cys Ala Pro Ser Arg Val
                240                 245                 250

agg agg ctc cct gat ggc cag ctg cag gtc acc tgg gag gac agc acc   997
Arg Arg Leu Pro Asp Gly Gln Leu Gln Val Thr Trp Glu Asp Ser Thr
255                 260                 265                 270

acc ggc aag gag gac acg ggc acc ttt gac acc gtc ctg tgg gcc ata   1045
Thr Gly Lys Glu Asp Thr Gly Thr Phe Asp Thr Val Leu Trp Ala Ile
                275                 280                 285

ggt cga gtc cca gac acc aga agt ctg aat ttg gag aag gct ggg gta   1093
Gly Arg Val Pro Asp Thr Arg Ser Leu Asn Leu Glu Lys Ala Gly Val
                290                 295                 300

gat act agc ccc gac act cag aag atc ctg gtg gac tcc cgg gaa gcc   1141
Asp Thr Ser Pro Asp Thr Gln Lys Ile Leu Val Asp Ser Arg Glu Ala
                305                 310                 315

acc tct gtg ccc cac atc tac gcc att ggt gac gtg gtg gag ggg cgg   1189
Thr Ser Val Pro His Ile Tyr Ala Ile Gly Asp Val Val Glu Gly Arg
                320                 325                 330
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cct gag ctg aca ccc aca gcg atc atg gcc ggg agg ctc ctg gtg cag   1237
Pro Glu Leu Thr Pro Thr Ala Ile Met Ala Gly Arg Leu Leu Val Gln
335             340             345                 350

cgg ctc ttc ggc ggg tcc tca gat ctg atg gac tac gac aat gtt ccc   1285
Arg Leu Phe Gly Gly Ser Ser Asp Leu Met Asp Tyr Asp Asn Val Pro
                355             360                 365

acg acc gtc ttc acc cca ctg gag tat ggc tgt gtg ggg ctg tcc gag   1333
Thr Thr Val Phe Thr Pro Leu Glu Tyr Gly Cys Val Gly Leu Ser Glu
                370             375                 380

gag gag gca gtg gct cgc cac ggg cag gag cat gtt gag gtc tat cac   1381
Glu Glu Ala Val Ala Arg His Gly Gln Glu His Val Glu Val Tyr His
        385             390                 395

gcc cat tat aaa cca ctg gag ttc acg gtg gct gga cga gat gca tcc   1429
Ala His Tyr Lys Pro Leu Glu Phe Thr Val Ala Gly Arg Asp Ala Ser
        400             405                 410

cag tgt tat gta aag atg gtg tgc ctg agg gag ccc cca cag ctg gtg   1477
Gln Cys Tyr Val Lys Met Val Cys Leu Arg Glu Pro Pro Gln Leu Val
415             420             425                 430

ctg ggc ctg cat ttc ctt ggc ccc aac gca ggc gaa gtt act caa gga   1525
Leu Gly Leu His Phe Leu Gly Pro Asn Ala Gly Glu Val Thr Gln Gly
                435             440                 445

ttt gct ctg ggg atc aag tgt ggg gct tcc tat gcg cag gtg atg cgg   1573
Phe Ala Leu Gly Ile Lys Cys Gly Ala Ser Tyr Ala Gln Val Met Arg
            450             455                 460

acc gtg ggt atc cat ccc aca tgc tct gag gag gta gtc aag ctg cgc   1621
Thr Val Gly Ile His Pro Thr Cys Ser Glu Glu Val Val Lys Leu Arg
            465             470                 475

atc tcc aag cgc tca ggc ctg gac ccc acg gtg aca ggc tgc tga ggg   1669
Ile Ser Lys Arg Ser Gly Leu Asp Pro Thr Val Thr Gly Cys Xaa Gly
        480             485                 490

taagcgccat ccctgcaggc cagggcacac ggtgcgcccg ccgccagctc ctcggaggcc 1729

agacccagga tggctgcagg ccaggtttgg ggggcctcaa ccctctcctg gagcgcctgt 1789

gagatggtca gcgtggagcg caagtgctgg acgggtggcc cgtgtgcccc acagggatgg 1849

ctcaggggac tgtccacctc acccctgcac ctttcagcct ttgccgccgg gcaccccccc 1909

caggctcctg gtgccggatg atgacgacct gggtggaaac ctaccctgtg ggcacccatg 1969

tccgagcccc ctggcatttc tgcaatgcaa ataaagaggg tactttttct gaagtgtgta 2029

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Gly Gly Ser Gly Gly Leu Ala Cys Ala Lys Glu Ala Ala Gln Leu Gly
             20                  25                  30

Arg Lys Val Ala Val Val Asp Tyr Val Glu Pro Ser Pro Gln Gly Thr
         35                  40                  45

Arg Trp Gly Leu Gly Gly Thr Cys Val Asn Val Gly Cys Ile Pro Lys
     50                  55                  60

Lys Leu Met His Gln Ala Ala Leu Leu Gly Gly Leu Ile Gln Asp Ala
 65                  70                  75                  80

Pro Asn Tyr Gly Trp Glu Val Ala Gln Pro Val Pro His Asp Trp Arg
             85                  90                  95

Lys Met Ala Glu Ala Val Gln Asn His Val Lys Ser Leu Asn Trp Gly
            100                 105                 110

His Arg Val Gln Leu Gln Asp Arg Lys Val Lys Tyr Phe Asn Ile Lys
        115                 120                 125

Ala Ser Phe Val Asp Glu His Thr Val Cys Gly Val Ala Lys Gly Gly
        130                 135                 140

Lys Glu Ile Leu Leu Ser Ala Asp His Ile Ile Ile Ala Thr Gly Gly
145                 150                 155                 160

Arg Pro Arg Tyr Pro Thr His Ile Glu Gly Ala Leu Glu Tyr Gly Ile
            165                 170                 175

Thr Ser Asp Asp Ile Phe Trp Leu Lys Glu Ser Pro Gly Lys Thr Leu
            180                 185                 190

Val Val Gly Ala Ser Tyr Val Ala Leu Glu Cys Ala Gly Phe Leu Thr
        195                 200                 205

Gly Ile Gly Leu Asp Thr Thr Ile Met Met Arg Ser Ile Pro Leu Arg
        210                 215                 220

Gly Phe Asp Gln Gln Met Ser Ser Met Val Ile Glu His Met Ala Ser
225                 230                 235                 240

His Gly Thr Arg Phe Leu Arg Gly Cys Ala Pro Ser Arg Val Arg Arg
            245                 250                 255
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```
Leu Pro Asp Gly Gln Leu Gln Val Thr Trp Glu Asp Ser Thr Thr Gly
            260             265             270

Lys Glu Asp Thr Gly Thr Phe Asp Thr Val Leu Trp Ala Ile Gly Arg
        275             280             285

Val Pro Asp Thr Arg Ser Leu Asn Leu Glu Lys Ala Gly Val Asp Thr
    290             295             300

Ser Pro Asp Thr Gln Lys Ile Leu Val Asp Ser Arg Glu Ala Thr Ser
305             310             315             320

Val Pro His Ile Tyr Ala Ile Gly Asp Val Val Glu Gly Arg Pro Glu
            325             330             335

Leu Thr Pro Thr Ala Ile Met Ala Gly Arg Leu Leu Val Gln Arg Leu
        340             345             350

Phe Gly Gly Ser Ser Asp Leu Met Asp Tyr Asp Asn Val Pro Thr Thr
        355             360             365

Val Phe Thr Pro Leu Glu Tyr Gly Cys Val Gly Leu Ser Glu Glu Glu
    370             375             380

Ala Val Ala Arg His Gly Gln Glu His Val Glu Val Tyr His Ala His
385             390             395             400

Tyr Lys Pro Leu Glu Phe Thr Val Ala Gly Arg Asp Ala Ser Gln Cys
            405             410             415

Tyr Val Lys Met Val Cys Leu Arg Glu Pro Pro Gln Leu Val Leu Gly
        420             425             430

Leu His Phe Leu Gly Pro Asn Ala Gly Glu Val Thr Gln Gly Phe Ala
        435             440             445

Leu Gly Ile Lys Cys Gly Ala Ser Tyr Ala Gln Val Met Arg Thr Val
    450             455             460

Gly Ile His Pro Thr Cys Ser Glu Glu Val Val Lys Leu Arg Ile Ser
465             470             475             480

Lys Arg Ser Gly Leu Asp Pro Thr Val Thr Gly Cys Xaa Gly
            485             490
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<213> Homo sapiens

<400> 5
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tggaaaccta ccctgtgggc acccatgtcc gagcccctg gcatttctgc aatgcaaata 120

aagagggtac   130

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<210> 6
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<212> DNA
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<220>
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<210> 7
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<212> DNA
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<220>
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<400> 7
gcgctcgagc tactatagag ttagattaag ac                                    32


<210> 8
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<212> DNA
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<220>
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<400> 8
tatgatctcc tggtggtc                                                    18


<210> 9
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<212> DNA
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<220>
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<400> 11
agaaggttcc acgtagtcca c   21

<210> 12
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<400> 12
ccatacgatg ttccagatta c   21

<210> 13
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<400> 13
acgatggcgg caatggcggt g   21

<210> 14
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accatggagg accaagcagg t   21

<210> 15
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ttaccctcag cagcctgtca c   21

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<220>
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gcgccatccc tgcaggccag g   21

<210> 17
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<400> 17
cacacttcag aaaaagtacc c   21

<210> 18
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<212> DNA
<213> Homo sapiens

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gccgtggcgg gcggggtgcg gggcgcggcg cggggcgcag cag .   103

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agtagacacg atgacacctt ttgcaggcta aaaaggctga gagtggcact atgtgcagtg 180

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<220>
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<222> (498)
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<400> 38
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Gln Tyr Gly Lys Lys Val Met Val Leu Asp Phe Val Thr Pro Thr Pro
        35                  40                  45

Leu Gly Thr Arg Trp Gly Leu Gly Gly Thr Cys Val Asn Val Gly Cys
    50                  55                  60

Ile Pro Lys Lys Leu Met His Gln Ala Ala Leu Leu Gly Gln Ala Leu
65                  70                  75                  80

Gln Asp Ser Arg Asn Tyr Gly Trp Lys Val Glu Glu Tyr Val Lys His
            85                  90                  95

Asp Trp Asp Arg Met Ile Glu Ala Val Gln Asn His Ile Gly Ser Leu
            100                 105                 110

Asn Trp Gly Tyr Arg Val Ala Leu Arg Glu Lys Lys Val Val Tyr Glu
        115                 120                 125

Asn Ala Tyr Gly Gln Phe Ile Gly Pro His Arg Ile Lys Ala Thr Asn
    130                 135                 140

Asn Lys Gly Lys Glu Lys Ile Tyr Ser Ala Glu Ser Phe Leu Ile Ala
145                 150                 155                 160

Thr Gly Glu Arg Pro Arg Tyr Leu Gly Ile Pro Gly Asp Lys Glu Tyr
            165                 170                 175

Cys Ile Ser Ser Asp Asp Leu Phe Ser Leu Pro Tyr Cys Pro Gly Lys
            180                 185                 190

Thr Leu Val Val Gly Ala Ser Tyr Val Ala Leu Glu Cys Ala Gly Phe
        195                 200                 205

Leu Ala Gly Ile Gly Leu Gly Val Thr Val Met Val Arg Ser Ile Leu
    210                 215                 220

Leu Arg Gly Phe Asp Gln Asp Met Ala Asn Lys Ile Gly Glu His Met
225                 230                 235                 240
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Glu Glu His Gly Ile Lys Phe Ile Arg Gln Phe Val Pro Ile Lys Val
                245             250             255

Glu Gln Ile Glu Ala Gly Thr Pro Gly Arg Leu Arg Val Val Ala Gln
            260             265             270

Ser Thr Asn Ser Glu Glu Ile Ile Glu Gly Glu Tyr Asn Thr Val Met
        275             280             285

Leu Ala Ile Gly Arg Asp Ala Cys Thr Arg Lys Ile Gly Leu Glu Thr
    290             295             300

Val Gly Val Lys Ile Asn Glu Lys Thr Gly Lys Ile Pro Val Thr Asp
305             310             315             320

Glu Glu Gln Thr Asn Val Pro Tyr Ile Tyr Ala Ile Gly Asp Ile Leu
            325             330             335

Glu Asp Lys Val Glu Leu Thr Pro Val Ala Ile Gln Ala Gly Arg Leu
            340             345             350

Leu Ala Gln Arg Leu Tyr Ala Gly Ser Thr Val Lys Cys Asp Tyr Glu
        355             360             365

Asn Val Pro Thr Thr Val Phe Thr Pro Leu Glu Tyr Gly Ala Cys Gly
    370             375             380

Leu Ser Glu Glu Lys Ala Val Glu Lys Phe Gly Glu Glu Asn Ile Glu
385             390             395             400

Val Tyr His Ser Tyr Phe Trp Pro Leu Glu Trp Thr Ile Pro Ser Arg
            405             410             415

Asp Asn Asn Lys Cys Tyr Ala Lys Ile Ile Cys Asn Thr Lys Asp Asn
            420             425             430

Glu Arg Val Val Gly Phe His Val Leu Gly Pro Asn Ala Gly Glu Val
        435             440             445

Thr Gln Gly Phe Ala Ala Ala Leu Lys Cys Gly Leu Thr Lys Lys Gln
    450             455             460

Leu Asp Ser Thr Ile Gly Ile His Pro Val Cys Ala Glu Val Phe Thr
465             470             475             480

Thr Leu Ser Val Thr Lys Arg Ser Gly Ala Ser Ile Leu Gln Ala Gly
            485             490             495

Cys Xaa Gly
```